In the Claims:

The claims, including amendments, should now read as follows:

1. – 30. (Canceled)

31. (Currently Amended) A process for detecting a single nucleotide polymorphism (SNP) in a target polynucleotide, comprising:

(a) contacting one or more allele specific oligonucleotide primers (P1) with one or more target polynucleotides (TP), wherein said target polynucleotide possesses a first portion that is complementary to a second portion located on said P1 at or near one end thereof but wherein ~~the terminal~~ nucleotide at said end, and third nucleotide from ~~the terminal nucleotide, at~~ said end ~~of said P1~~ may not be complementary to the corresponding nucleotide of said target polynucleotide, and wherein such contacting occurs under conditions that promote hybridization between the first and second portions thereby forming ~~an~~ a P1-TP complex and wherein P1 comprises the nucleotide sequence of SEQ ID NO: 13;

(b) contacting the P1-TP complex of (a) with an exonuclease deficient deoxyribonucleotide (DNA) polymerase enzyme under conditions that promote extension of the P1 with the TP as template thereby forming an extended segment (ES) of P1 only when the terminal nucleotide at the end of P1 is complementary to the corresponding nucleotide of TP; and

(c) detecting the extended P1

thereby detecting an SNP in said target polynucleotide.

32. (Currently Amended) A method for determining the presence of a single nucleotide polymorphism (SNP) in a target polynucleotide comprising:

(a) contacting an allele specific oligonucleotide primer (P1) with a target polynucleotide (TP), under conditions supporting hybridization between P1 and TP,

wherein said TP possesses a portion complementary to a segment of P1 at or near one end of P1 but wherein the ~~terminal~~ nucleotide at said end, and third nucleotide from ~~the terminal nucleotide, at~~ said ~~one~~ end ~~of said P1~~ may independently be non-complementary to the corresponding nucleotide of TP and forming a P1-TP hybridized complex;

(b) contacting the P1-TP complex of (a) with an exonuclease deficient deoxyribonucleotide (DNA) polymerase enzyme under conditions supporting extension of P1 with TP as template to form an extended segment (ES) of P1 only when the terminal nucleotide at the end of P1 is complementary to the corresponding nucleotide of TP;

(c) determining the extended P1 by removing the target polynucleotide from the complex formed in step (b) and contacting a primer oligonucleotide (P2) with the extended P1, wherein P2 comprises a portion that hybridizes to the extended segment of P1 and a portion that does not and then contacting an amplification target circle (ATC) with said P1-P2 wherein the ATC hybridizes to the portion of P2 that does not hybridize to extended P1 and under conditions promoting rolling circle amplification of the ATC with P2 as primer thereby extending P2 to form TS-DNA

wherein said method does not include a ligation reaction and

whereby TS-DNA formation indicates extension of P1 in step ~~(c)~~ (b) and thus the presence or absence of a polymorphism in TG.

33. (Previously Presented) The method of claim 32 wherein P2 comprises two 3'-ends.

34. (Previously Presented) The method of claim 32 wherein the target polynucleotide is derived from genomic DNA.

35. (Previously Presented) The method of claim 34 wherein the genomic DNA comprises human genomic DNA.

36. (Previously Presented) The method of claim 34 wherein the genomic DNA comprises non-human genomic DNA.

37. (Previously Presented) The method of claim 32 wherein the exonuclease-deficient DNA polymerase is T7 Sequenase or Tth polymerase.

38. (Previously Presented) The method of claim 32 wherein P1 is attached to a solid support.

39. (Previously Presented) The process of claim 38 wherein the solid support is composed of at least one member selected from the group consisting of acrylamide, cellulose, nitrocellulose, glass, polystyrene, polyethylene vinyl acetate, polypropylene, polymethacrylate, polyethylene, polyethylene oxide, glass, polysilicates, polycarbonates, teflon, fluorocarbons, nylon, silicon rubber, polyanhydrides, polyglycolic acid, polylactic acid, polyorthoesters, polypropylfumerate, collagen, glycosaminoglycans, and polyamino acids.

40. (Previously Presented) The method of claim 38 wherein the solid support is made of glass or plastic.

41. (Previously Presented) The process of claim 32 wherein P1 is selected from the group consisting of the sequences of SEQ ID NOs: 1, 2, 3, 4, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, and 26.

42. (Previously Presented) A method for diagnosing a disease characterized by a mutated gene sequence comprising:

(a) obtaining a sample of a mutated gene sequence from an animal afflicted with said disease; and

(b) applying the method of claim 32 wherein at least a portion of said mutated gene sequence is used as either the target polynucleotide (TP) or the allele specific oligonucleotide (P1).

43. (Previously Presented) The method of claim 42 wherein the mutated gene sequence is used as the target polynucleotide.

44. (Previously Presented) The method of claim 42 wherein said animal is a human.

45. (Previously Presented) The method of claim 42 wherein said disease is a disease caused by, induced by or related to a mutation in at least one gene.

46. (Previously Presented) The method of claim 45 wherein said disease is a member selected from the group consisting of Parkinson's disease, Duchenne muscular dystrophy, Niemann-Pick disease, polyposis, neurofibromatosis, polycystic kidney disease, Tay-Sachs disease, xeroderma pigmentosa, ataxia-telangiectasia, Huntington disease, Li-Fraumeni syndrome, beta-thalassemia, sickle cell anemia, hemoglobin C disease, hemophilia, acute intermittent porphyria, cystic fibrosis, diabetes, obesity and cancer.

47. (Previously Presented) The method of claim 46 wherein said cancer is a member selected from the group consisting of leukemia, lymphoma, melanoma, neuroblastoma, retinoblastoma, rhabdomyosarcoma, Ewing sarcoma, head and neck cancer, skin cancer, brain cancer, esophageal cancer, stomach cancer, lung cancer, breast cancer, colon cancer, ovarian cancer, testicular cancer and prostate cancer.

48. (Previously Presented) The method of claim 32 wherein the third nucleotide from the end of said P1 is complementary to the corresponding nucleotide of the target polynucleotide.

49. (Previously Presented) The method of claim 32 wherein the third nucleotide from the end of said P1 is not complementary to the corresponding nucleotide of TP.

50. (Previously Presented) The method of claim 32 wherein both the terminal nucleotide and third nucleotide from the end of P1 are not complementary to the corresponding nucleotide of TP.